RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/587,804_
Source: _IFWP_
Date Processed by STIC: _8/8/06_

ENTERED

RAW SEQUENCE LISTING   DATE: 08/08/2006
PATENT APPLICATION: US/10/587,804   TIME: 09:07:30

Input Set : A:\0279woSEQ.ST25.txt
Output Set: N:\CRF4\08082006\J587804.raw

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   3 <110> APPLICANT: Maxygen Holdings Ltd.
   4        Maxygen ApS
   5        Bouquin, Thomas
   7 <120> TITLE OF INVENTION: Regulated Stop Codon Readthrough
   9 <130> FILE REFERENCE: 0279wo310
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/587,804
C--> 12 <141> CURRENT FILING DATE: 2006-07-31
  14 <150> PRIOR APPLICATION NUMBER: US 60/540,820
  15 <151> PRIOR FILING DATE: 2004-01-30
  17 <150> PRIOR APPLICATION NUMBER: US 60/631,306
  18 <151> PRIOR FILING DATE: 2004-11-29
  20 <160> NUMBER OF SEQ ID NOS: 27
  22 <170> SOFTWARE: PatentIn version 3.2
  24 <210> SEQ ID NO: 1
  25 <211> LENGTH: 1524
  26 <212> TYPE: DNA
  27 <213> ORGANISM: Artificial
  29 <220> FEATURE:
  30 <223> OTHER INFORMATION: PC-GPI cassette
  33 <220> FEATURE:
  34 <221> NAME/KEY: exon
  35 <222> LOCATION: (1)..(1518)
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  40 1               5                   10                  15
  42 tcc ggc aca cca gct cct ctt gac tca gtg ttc tcc agc agc gag cgt       96
  43 Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg
  44             20                  25                  30
  46 gcc cac cag gtg ctg cgc atc cgc aaa cgt gcc aac tcc ttc ctg gag      144
  47 Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu
  48         35                  40                  45
  50 gag ctc cgt cac agc agc ctg gag cgg gag tgc ata gag gag atc tgt      192
  51 Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys
  52     50                  55                  60
  54 gac ttc gag gag gcc aag gaa att ttc caa aat gtg gat gac aca ctg      240
  55 Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu
  56 65                  70                  75                  80
  58 gcc ttc tgg tcc aag cac gtc gac ggt gac cag tgc ttg gtc ttg ccc      288
  59 Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro
  60                 85                  90                  95
  62 ttg gag cac ccg tgc gcc agc ctg tgc tgc ggg cac ggc acg tgc atc      336
  63 Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile
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64            100              105              110
66 gac ggc atc ggc agc ttc agc tgc gac tgc cgc agc ggc tgg gag ggc      384
67 Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly
68            115              120              125
70 cgc ttc tgc cag cgc gag gtg agc ttc ctc aat tgc tcg ctg gac aac      432
71 Arg Phe Cys Gln Arg Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn
72        130              135              140
74 ggc ggc tgc acg cat tac tgc cta gag gag gtg ggc tgg cgg cgc tgt      480
75 Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys
76 145              150              155              160
78 agc tgt gcg cct ggc tac aag ctg ggg gac gac ctc ctg cag tgt cac      528
79 Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His
80            165              170              175
82 ccc gca gtg aag ttc cct tgt ggg agg ccc tgg aag cgg atg gag aag      576
83 Pro Ala Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys
84            180              185              190
86 aag cgc agt cac ctg aaa cga gac aca gaa gac caa gaa gac caa gta      624
87 Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val
88            195              200              205
90 gat ccg cgg ctc att gat ggg aag atg acc agg cgg gga gac agc ccc      672
91 Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro
92        210              215              220
94 tgg cag gtg gtc ctg ctg gac tca aag aag aag ctg gcc tgc ggg gca      720
95 Trp Gln Val Val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala
96 225              230              235              240
98 gtg ctc atc cac ccc tcc tgg gtg ctg aca gcg gcc cac tgc atg gat      768
99 Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp
100              245              250              255
102 gag tcc aag aag ctc ctt gtc agg ctt gga gag tat gac ctg cgg cgc     816
103 Glu Ser Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg
104              260              265              270
106 tgg gag aag tgg gag ctg gac ctg gac atc aag gag gtc ttc gtc cac     864
107 Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys Glu Val Phe Val His
108              275              280              285
110 ccc aac tac agc aag agc acc acc gac aat gac atc gca ctg ctg cac     912
111 Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His
112        290              295              300
114 ctg gcc cag ccc gcc acc ctc tcg cag acc ata gtg ccc atc tgc ctc     960
115 Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu
116 305              310              315              320
118 ccg gac agc ggc ctt gca gag cgc gag ctc aat cag gcc ggc cag gag    1008
119 Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu
120              325              330              335
122 acc ctc gtg acg ggc tgg gga tat cac agc agc cga gag aag gag gcc    1056
123 Thr Leu Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala
124        340              345              350
126 aag aga aac cgc acc ttc gtc ctc aac ttc atc aag att ccc gtg gtc    1104
127 Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val
128        355              360              365
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130 ccg cac aat gag tgc agc gag gtc atg agc aac atg gtg tct gag aac      1152
131 Pro His Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn
132     370                 375                 380
134 atg ctg tgt gcg ggc atc ctc ggg gac cgg cag gat gcc tgc gag ggc      1200
135 Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly
136 385                 390                 395                 400
138 gac agt ggg ggg ccc atg gtc gcc tcc ttc cac ggc acc tgg ttc ctg      1248
139 Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu
140                 405                 410                 415
142 gtg ggc ctg gtg agc tgg ggt gag ggc tgt ggg ctc ctt cac aac tac      1296
143 Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr
144                 420                 425                 430
146 ggc gtt tac acc aaa gtc agc cgc tac ctc gac tgg att cat ggg cac      1344
147 Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His
148                 435                 440                 445
150 atc aga gac aag gaa gcc ccc cag aag agc tgg gca cct ctg gaa ccc      1392
151 Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala Pro Leu Glu Pro
152     450                 455                 460
154 acg tac tgc gac ctc gcc cct ccc gct ggc acg acc gat gcc gct cac      1440
155 Thr Tyr Cys Asp Leu Ala Pro Pro Ala Gly Thr Thr Asp Ala Ala His
156 465                 470                 475                 480
158 cct ggc cgg agc gtc gtg cct gcc ctc ctg cct ctg ctc gcc ggg acc      1488
159 Pro Gly Arg Ser Val Val Pro Ala Leu Leu Pro Leu Leu Ala Gly Thr
160                 485                 490                 495
162 ctc ctg ctc ctg gaa acc gct acc gct ccc tagtaa                       1524
163 Leu Leu Leu Leu Glu Thr Ala Thr Ala Pro
164                 500                 505
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 1533
169 <212> TYPE: DNA
170 <213> ORGANISM: Artificial
172 <220> FEATURE:
173 <223> OTHER INFORMATION: PC-UAAC-GPI-4Stop cassette
176 <220> FEATURE:
177 <221> NAME/KEY: exon
178 <222> LOCATION: (1)..(1521)
179 <223> OTHER INFORMATION: 1384-1386: TAA stop codon
181 <400> SEQUENCE: 2
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183 Met Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile
184 1                 5                 10                 15
186 tcc ggc aca cca gct cct ctt gac tca gtg ttc tcc agc agc gag cgt      96
187 Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg
188                 20                 25                 30
190 gcc cac cag gtg ctg cgc atc cgc aaa cgt gcc aac tcc ttc ctg gag      144
191 Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu
192     35                 40                 45
194 gag ctc cgt cac agc agc ctg gag cgg gag tgc ata gag gag atc tgt      192
195 Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys
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Input Set : A:\0279woSEQ.ST25.txt
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196     50                  55                  60
198 gac ttc gag gag gcc aag gaa att ttc caa aat gtg gat gac aca ctg     240
199 Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu
200 65                  70                  75                  80
202 gcc ttc tgg tcc aag cac gtc gac ggt gac cag tgc ttg gtc ttg ccc     288
203 Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro
204                 85                  90                  95
206 ttg gag cac ccg tgc gcc agc ctg tgc tgc ggg cac ggc acg tgc atc     336
207 Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile
208                 100                 105                 110
210 gac ggc atc ggc agc ttc agc tgc gac tgc cgc agc ggc tgg gag ggc     384
211 Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly
212             115                 120                 125
214 cgc ttc tgc cag cgc gag gtg agc ttc ctc aat tgc tcg ctg gac aac     432
215 Arg Phe Cys Gln Arg Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn
216         130                 135                 140
218 ggc ggc tgc acg cat tac tgc cta gag gag gtg ggc tgg cgg cgc tgt     480
219 Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys
220 145                 150                 155                 160
222 agc tgt gcg cct ggc tac aag ctg ggg gac gac ctc ctg cag tgt cac     528
223 Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His
224             165                 170                 175
226 ccc gca gtg aag ttc cct tgt ggg agg ccc tgg aag cgg atg gag aag     576
227 Pro Ala Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys
228             180                 185                 190
230 aag cgc agt cac ctg aaa cga gac aca gaa gac caa gaa gac caa gta     624
231 Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val
232             195                 200                 205
234 gat ccg cgg ctc att gat ggg aag atg acc agg cgg gga gac agc ccc     672
235 Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro
236 210                 215                 220
238 tgg cag gtg gtc ctg ctg gac tca aag aag aag ctg gcc tgc ggg gca     720
239 Trp Gln Val Val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala
240 225                 230                 235                 240
242 gtg ctc atc cac ccc tcc tgg gtg ctg aca gcg gcc cac tgc atg gat     768
243 Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp
244             245                 250                 255
246 gag tcc aag aag ctc ctt gtc agg ctt gga gag tat gac ctg cgg cgc     816
247 Glu Ser Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg
248             260                 265                 270
250 tgg gag aag tgg gag ctg gac ctg gac atc aag gag gtc ttc gtc cac     864
251 Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys Glu Val Phe Val His
252             275                 280                 285
254 ccc aac tac agc aag agc acc acc gac aat gac atc gca ctg ctg cac     912
255 Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His
256         290                 295                 300
258 ctg gcc cag ccc gcc acc ctc tcg cag acc ata gtg ccc atc tgc ctc     960
259 Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu
260 305                 310                 315                 320
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RAW SEQUENCE LISTING   DATE: 08/08/2006
PATENT APPLICATION: **US/10/587,804**   TIME: 09:07:30

Input Set : **A:\0279woSEQ.ST25.txt**
Output Set: **N:\CRF4\08082006\J587804.raw**

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262 ccg gac agc ggc ctt gca gag cgc gag ctc aat cag gcc ggc cag gag     1008
263 Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu
264             325                 330                 335
266 acc ctc gtg acg ggc tgg gga tat cac agc agc cga gag aag gag gcc     1056
267 Thr Leu Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala
268             340                 345                 350
270 aag aga aac cgc acc ttc gtc ctc aac ttc atc aag att ccc gtg gtc     1104
271 Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val
272             355                 360                 365
274 ccg cac aat gag tgc agc gag gtc atg agc aac atg gtg tct gag aac     1152
275 Pro His Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn
276     370                 375                 380
278 atg ctg tgt gcg ggc atc ctc ggg gac cgg cag gat gcc tgc gag ggc     1200
279 Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly
280 385                 390                 395                 400
282 gac agt ggg ggg ccc atg gtc gcc tcc ttc cac ggc acc tgg ttc ctg     1248
283 Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu
284                 405                 410                 415
286 gtg ggc ctg gtg agc tgg ggt gag ggc tgt ggg ctc ctt cac aac tac     1296
287 Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr
288             420                 425                 430
290 ggc gtt tac acc aaa gtc agc cgc tac ctc gac tgg att cat ggg cac     1344
291 Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His
292             435                 440                 445
294 atc aga gac aag gaa gcc ccc cag aag agc tgg gca cct taa ctg gaa     1392
295 Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala Pro  ·  Leu Glu
296     450                 455                 460
298 ccc acg tac tgc gac ctc gcc cct ccc gct ggc acg acc gat gcc gct     1440
299 Pro Thr Tyr Cys Asp Leu Ala Pro Pro Ala Gly Thr Thr Asp Ala Ala
300     465                 470                 475
302 cac cct ggc cgg agc gtc gtg cct gcc ctc ctg cct ctg ctc gcc ggg     1488
303 His Pro Gly Arg Ser Val Val Pro Ala Leu Leu Pro Leu Leu Ala Gly
304 480                 485                 490                 495
306 acc ctc ctg ctc ctg gaa acc gct acc gct ccc tagtaatagt ga          1533
307 Thr Leu Leu Leu Leu Glu Thr Ala Thr Ala Pro
308             500                 505
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311 <210> SEQ ID NO: 3
312 <211> LENGTH: 1533
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial
316 <220> FEATURE:
317 <223> OTHER INFORMATION: PC-UGAC-GPI-4Stop cassette
320 <220> FEATURE:
321 <221> NAME/KEY: exon
322 <222> LOCATION: (1)..(1521)
324 <400> SEQUENCE: 3

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325 atg tgg cag ctc aca agc ctc ctg ctg ttc gtg gcc acc tgg gga att     48
326 Met Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile
327 1               5                   10                  15
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/08/2006
PATENT APPLICATION: US/10/587,804   TIME: 09:07:31

Input Set : A:\0279woSEQ.ST25.txt
Output Set: N:\CRF4\08082006\J587804.raw

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27

VERIFICATION SUMMARY   DATE: 08/08/2006
PATENT APPLICATION: US/10/587,804   TIME: 09:07:31

Input Set : **A:\0279woSEQ.ST25.txt**
Output Set: **N:\CRF4\08082006\J587804.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date